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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/380,203

DATE: 06/07/2000
TIME: 14:14:47

Input Set : A:\seqlist- 0609 4370001.txt
Output Set: N:\CRF3\06072000\I380203.raw

ENTERED

4 (1) GENERAL INFORMATION:
C--> 6 (i) APPLICANT: de la Monte, Suzanne
7 Wands, Jack R.
9 (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
10 Screening Drugs Effective for the Treatment or Prevention
11 of Alzheimer's Disease
13 (iii) NUMBER OF SEQUENCES: 14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
17 (B) STREET: 1100 New York Ave., Suite 600
18 (C) CITY: Washington
19 (D) STATE: DC
20 (E) COUNTRY: USA
21 (F) ZIP: 20005-3934
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
C--> 29 (vi) CURRENT APPLICATION DATA:
C--> 30 (A) APPLICATION NUMBER: US/09/380,203
C--> 31 (B) FILING DATE: 25-Apr-2000
32 (C) CLASSIFICATION:
38 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: PCT/US98/03685
36 (B) FILING DATE: 26-FEB-1998
39 (A) APPLICATION NUMBER: US 60/038,908
40 (B) FILING DATE: 26-FEB-1997
42 (viii) ATTORNEY/AGENT INFORMATION:
43 (A) NAME: Esmond, Robert W.
44 (B) REGISTRATION NUMBER: 32,893
45 (C) REFERENCE/DOCKET NUMBER: 0609.4370001
47 (ix) TELECOMMUNICATION INFORMATION:
48 (A) TELEPHONE: 202-371-2600
49 (B) TELEFAX: 202-371-2540
52 (2) INFORMATION FOR SEQ ID NO: 1:
54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 1442 base pairs
56 (B) TYPE: nucleic acid
57 (C) STRANDEDNESS: double
58 (D) TOPOLOGY: both
60 (ii) MOLECULE TYPE: cdna
63 (ix) FEATURE:
64 (A) NAME/KEY: CDS
65 (B) LOCATION: 15..1139
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
70 TTTT TTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC

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71      Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
72      1      5      10
74 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC      98
75 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser
76      15      20      25
78 GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC      146
79 Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys
80      30      35      40
82 ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT      194
83 Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe
84 45      50      55      60
86 CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC      242
87 Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro
88      65      70      75
90 TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC      290
91 Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala
92      80      85      90
94 CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG      338
95 Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met
96      95      100      105
98 TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC      386
99 Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu
100     110     115     120
102 CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT      434
103 Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile
104 125     130     135     140
106 TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG      482
107 Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val
108     145     150     155
110 CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG      530
111 Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys
112     160     165     170
114 CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC      578
115 His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His
116     175     180     185
118 CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG      626
119 His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln
120     190     195     200
122 AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC      674
123 Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly
124 205     210     215     220
126 TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC      722
127 Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser
128     225     230     235
130 CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT      770
131 Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe
132     240     245     250
134 TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC      818
135 Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile

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136          255          260          265
138 TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT      866
139 Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala
140          270          275          280
142 GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT      914
143 Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys
144 285          290          295          300
146 TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG      962
147 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp
148          305          310          315
150 CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC      1010
151 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
152          320          325          330
154 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA      1058
155 Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro
156          335          340          345
158 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT      1106
159 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
160          350          355          360
162 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT      1159
163 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
164 365          370          375
166 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA      1219
168 AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT      1279
170 CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTSTA AACAGTTACA      1339
172 TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA      1399
174 GTAACAGAGT TCTTTTATAA CTTTAAACA AAGCTTTAGA GCA      1442
177 (2) INFORMATION FOR SEQ ID NO: 2:
179 (i) SEQUENCE CHARACTERISTICS:
180 (A) LENGTH: 375 amino acids
181 (B) TYPE: amino acid
182 (D) TOPOLOGY: linear
184 (ii) MOLECULE TYPE: protein
186 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
188 Met Glu Phe Ser Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
189 1 5 10 15
191 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
192 20 25 30
194 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
195 35 40 45
197 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
198 50 55 60
200 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
201 65 70 75 80
203 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His Ala Arg Leu Cys Leu
204 85 90 95
206 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
207 100 105 110
209 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp

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210          115          120          125
212 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
213          130          135          140
215 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
216 145          150          155          160
218 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
219          165          170          175
221 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
222          180          185          190
224 Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
225          195          200          205
227 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
228          210          215          220
230 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
231 225          230          235          240
233 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
234          245          250          255
236 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
237          260          265          270
239 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
240          275          280          285
242 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
243          290          295          300
245 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
246 305          310          315          320
248 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
249          325          330          335
251 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
252          340          345          350
254 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
255          355          360          365
257 Ser Gln Thr Pro Asp Leu Arg
258          370          375

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260 (2) INFORMATION FOR SEQ ID NO: 3:

262 (i) SEQUENCE CHARACTERISTICS:

263 (A) LENGTH: 1381 base pairs

264 (B) TYPE: nucleic acid

265 (C) STRANDEDNESS: double

266 (D) TOPOLOGY: both

268 (ii) MOLECULE TYPE: cDNA

273 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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275 TTTT TTTT TTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT    60
277 CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC    120
279 AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTT TTAGTA    180
281 GAGATGGAGT TTAACCCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC    240
283 TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGCCTC    300
285 TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCACCTGA TGTGCCCCAA GCTGGTCTCC    360
287 TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCCTCAGCC    420
289 GTGCCTGGCC TTTT TATTTT ATTTT TTTTA AGACACAGGT GTACCACTCT TACCCAGGAT    480

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291 GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540
293 TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600
295 TTTATTTTAA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660
297 AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC 720
299 CCAGCTCCTT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTGTGTAT 780
301 TTTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTTGA TCTTGATCTC TTGACCTTGT 840
303 GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCTGTGACT CCACGCCGGC 900
305 CTATTTTAA TTTTGTGTTG TTTGAAATGG AATCTCACTC TGTACCCAG GTGGGAGTGC 960
307 AATGGCAAA CTGCGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCTGTCTC 1020
309 AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCGCTAATT TTTGTATTTT 1080
311 CATTAGAGGC GGGTTTACCA TATTGTGTAG GCTGGGTCTC AACTCTCTGA CCTCAGGTGA 1140
313 CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
315 GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
317 TCAAACTTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320
319 TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380
321 C 1381
323 (2) INFORMATION FOR SEQ ID NO: 4:
325 (i) SEQUENCE CHARACTERISTICS:
326 (A) LENGTH: 1418 base pairs
327 (B) TYPE: nucleic acid
328 (C) STRANDEDNESS: both
329 (D) TOPOLOGY: both
331 (ii) MOLECULE TYPE: cDNA
336 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
338 TTTTTCCTTTT GAGATGGAGT TTTCTGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT 60
340 CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
342 AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTCCTAGT 180
344 AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT 240
346 CCCGTCTCGG CCTCCCAAGG TGCTAGATAC AGGACTGAGC ACCATGCCCG GCCTCTGCCT 300
348 GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT 360
350 CAAGCAGTCC ACCTGCCTCA GCCTCCCAAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC 420
352 TGGCCTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480
354 GCACTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540
356 TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTAT 600
358 TTTTATTTT ATTTTGTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660
360 GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG 720
362 CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCTA GCTAATTTT TGTATTTT 780
364 AGTAGAGATG GGGTTTCACC ATGTTCCGCA GGTGTGATGCT AGATCTCTTG ACCTGTGTAT 840
366 CTGCCCTGCC CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC 900
368 TATTTTAAAT TTTTGTGTTG TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA 960
370 ATGGCCAAAT CTGCGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT 1020
372 CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCGCTAA TTTTGTATT 1080
374 TTCATTAGAG GCGGGGTTTC ACCATATTG TCAGGCTGGT CTCAAACCTC TGACCTCAGG 1140
376 TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGCGTGACGC CTCACCCAGC 1200
378 CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGTC TTGCTATGTT GCCCAGGCTG 1260
380 GTCTCAAACT TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC 1320
382 ATTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG 1380
384 AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT 1418
386 (2) INFORMATION FOR SEQ ID NO: 5:

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VERIFICATION SUMMARY DATE: 06/07/2000
PATENT APPLICATION: US/09/380,203 TIME: 14:14:48

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L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]